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Exact Entropy of Tightly Double Folded Ring Polymers allows for Multi-scale Modeling of Genomes

Randomly branching polymers provide a valuable framework for studying genome organization: Tree-like double-folded structures of ring polymers in melt conditions [1,2] resemble eukaryotic DNA during interphase on scales above several kilo base pairs [3,4]. Moreover, extensive supercoiling causes circular bacterial DNA to adopt branched structures [5]. Much of the structural complexity of branched polymers can be captured using low parameter models. Our model in particular uses a single parameter, the branching activity, to tune the degree of branching in our samples. The branching activity determines together with an entropic contribution residing in the annealed connectivity of tree-nodes how much branching we observe in our samples. In my presentation, I will show how the latter entropic contribution can be computed exactly, at least in ideal systems. Our methods apply both to branched polymers and tightly double folded ring polymers. Knowledge about the full partition function of the system then allows to 1) sample branched polymers in linear time, 2) sample tightly double folded rings efficiently using algorithms specialized for simulating trees [6], 3) compute statistical averages analytically. As I will argue, our work shows that the branching activity can be used as a scaling parameter: Bigger trees with relatively low branching activity correspond to fine-grained versions of small trees with relatively high branching activity. This paves the way for a multi-scale modeling approach of genomic organization and in the last part of my presentation I will discuss what our findings imply for hi-C data of bacterial chromosomes.

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Role

Master/PhD student

Primary author(s) : Mr. VAN DER HOEK, Pieter Hendrik Willem (Scuola Internazionale di Studi Avanzati (SISSA))

Presenter(s): Mr. VAN DER HOEK, Pieter Hendrik Willem (Scuola Internazionale di Studi Avanzati (SISSA))